

## CLAIMS

What is claimed is:

1. A method for identifying a repeat sequence, the method comprising the steps of:
  - selecting a query sequence;
  - testing said query sequence with a redundant file;
  - identifying sequences in the redundant file that contain a similar sequence to a portion of the query sequence, wherein said identified sequences and said similar portion of the query sequence make up a pairwise sequence alignment;
  - aligning all the identified pairwise sequence alignments;
  - designating the right and left endpoints of each identified sequence and any intervening sequences;
  - identifying a position within the query sequence corresponding to each endpoint;
  - defining regions within the query sequence, wherein a region is a sequence between two consecutive positions matching two endpoints; and
  - identifying each regions having at least five sequence matches in the identified pairwise alignments as a repeat sequence.
2. A method for constructing a repeat database comprising:
  - selecting a query sequence;
  - selecting known repeat sequences;
  - adding known repeat sequences into a repeat sequence database;
  - masking said query sequence with repeat sequences in the repeat sequence database;
  - testing said masked query sequence with a redundant file;

1 identifying sequences in the redundant file that contain a similar sequence to a portion of  
2 the query sequence, wherein said identified sequences and said similar portion of the query  
3 sequence make up a pairwise sequence alignment;

4 aligning all the identified pairwise sequence alignments;

5 designating the right and left endpoints of each identified sequence and any intervening  
6 sequences;

7 identifying a position within the query sequence corresponding to each endpoint;

8 defining regions within the query sequence, wherein a region is a sequence between two  
9 consecutive positions matching two endpoints;

10 identifying any two successive regions having a large variance in the number of sequence  
11 matches; and

12 adding the sequence within the region of the two successive regions having the highest  
13 number of sequence matches into the repeat sequence database.

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15 3. The method of claim 2, wherein the large variance in the number of sequence matches is  
16 equal to 5 or more.

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18 4. A database product of the process of claim 2.

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20 5. The method of claim 1 or 2, wherein said sequence is a deoxyribonucleotide sequence.

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22 6. The method of claim 1 or 2, wherein said sequence is a ribonucleotide sequence.

1 7. The method of claim 1 or 2, wherein said sequences are derived from animal DNA or  
2 RNA.

4 8. The method of claim 7, wherein said animal is a human.

6 9. The method of claim 8, wherein said animal is a mouse.

8 10. The method of claim 1 or 2, wherein said sequences are derived from plant DNA or  
9 RNA.

11 11. The method of claim 10, wherein said plant is a single-cell plant.

13 12. The method of claim 1 or 2, wherein said sequences are derived from fungal DNA or  
14 RNA.

16 13. The method of claim 1 or 2, wherein said sequences are derived from DNA or RNA of a  
17 microorganism or virus.

19 14. The method of claim 1 or 2, wherein said sequences are derived from DNA or RNA of a  
20 single-cell eukaryote.

22 15. The method of claim 1 or 2, wherein said sequences are derived from synthetic man-  
23 made DNA or RNA.

1 16. The method of claim 1 or 2, wherein said sequences are postulated based upon amino  
2 acid sequences.

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4 17. The method of claim 2, wherein said database is encoded in a biological medium.

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6 18. The method of claim 2, wherein said database is encoded in a written medium.

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8 19. The method of claim 2, wherein said database is encoded in an electronic medium.

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10 20. The method of claim 19, wherein said electronic medium is a computer-readable  
11 medium.

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13 21. The method of claim 20, wherein said computer-readable medium is addressable through  
14 an internet connection.

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16 22. The method of claim 1 or 2, wherein said redundant file is a Public Domain Database.

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18 23. The method of claim 22, wherein said Public Domain Database is GenBank.

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20 24. The method of claim 22, wherein said Public Domain Database is dbEST.

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22 25. The method of claim 22, wherein said Public Domain Database is TIGR.

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24 26. The method of claim 22, wherein said Public Domain Database is SwissProt.

1 27. The method of claim 1 or 2, wherein sequence comparisons are carried out using a  
2 Database Search Algorithm.

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4 28. The method of claim 27, wherein said Database Search Algorithm is BLAST.

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6 29. The method of claim 27, wherein said Database Search Algorithm is FASTA.

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8 30. The method of claim 27, wherein said Database Search Algorithm is Smith-Waterman.

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10 31. The method of claim 1 or 2, wherein said sequence comparisons are carried out utilizing  
11 a Scoring Matrix Program.

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13 32. The method of claim 31, wherein said Scoring Matrix Program is PAM.

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15 33. The method of claim 31, wherein said Scoring Matrix Program is BLOSUM.

16  
17 34. The process of Figure 2.

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19 35. A repeat sequence product of the process of claim 1.

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21 36. A kit for analyzing nucleotide sequences comprising:

22 an electronic medium readable by a computer, said medium encoding a database  
23 produced by the method of claim 2.

24  
25 37. A kit for analyzing nucleotide sequences comprising:

1 an electronic medium readable by a computer, said medium encoding a database  
2 produced by the method of claim 2; and,  
3 instructions for the use of said database.  
4

5 38. A kit for analyzing nucleotide sequences comprising:

6 an electronic medium readable by a computer, said medium encoding a database  
7 produced by the method of claim 2;  
8 instructions for the use of said database; and,  
9 a computer.  
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11 39. An improved database of nucleotide sequences, the improvement consisting of repeat  
12 sequences containing a similar sequence to a portion of a query sequence, wherein said identified  
13 sequences and said similar portion of the query sequence make up a pairwise sequence  
14 alignment, and wherein all identified pairwise sequence alignments have right and left endpoints  
15 of each identified sequence and any intervening sequences.